

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 21, 2007, 08:55:29 ; Search time 167 Seconds
(without alignments)
38.092 Million cell updates/sec

Title: US-10-766-735A-125-X-IS-PHE
Perfect score: 93
Sequence: 1 CCEfCCNPACTGC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	93	100.0	13	9	AEC92586	Aec92586 Gastroint
	2	93	100.0	14	8	ADR48470	Adr48470 GC-C acti
	3	93	100.0	14	8	ADR48323	Adr48323 GC-C acti
	4	93	100.0	14	9	AEC92920	Aec92920 Gastroint
	5	93	100.0	14	9	AEC92919	Aec92919 Gastroint
	6	93	100.0	14	9	AEC92921	Aec92921 Gastroint

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Title: US-10-766-735A-125-X-IS-TRP
Perfect score: 98
Sequence: 1 CCEwCCNPACTGC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID	Description	
1	98	100.0	13	9	AEC92590	Aec92590 Gastroint	
2	98	100.0	14	8	ADR48474	Adr48474 GC-C acti	
3	98	100.0	14	8	ADR48327	Adr48327 GC-C acti	
4	98	100.0	14	9	AEC92903	Aec92903 Gastroint	
5	98	100.0	14	9	AEC92905	Aec92905 Gastroint	
6	98	100.0	14	9	AEC92894	Aec92894 Gastroint	

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Run on: April 21, 2007, 08:55:29 ; Search time 167 Seconds
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Title: US-10-766-735A-125-X-IS-TYR
Perfect score: 94
Sequence: 1 CCEyCCNPACTGC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length	DB	ID	Description
1	94	100.0	13	9	AEC92573	Aec92573 Gastroint
2	94	100.0	13	9	AEC93229	Aec93229 Gastroint
3	94	100.0	14	8	ADR48364	Adr48364 Analgesic
4	94	100.0	14	9	AEC92739	Aec92739 Gastroint
5	94	100.0	14	9	AEC92731	Aec92731 Gastroint
6	94	100.0	14	9	AEC92732	Aec92732 Gastroint